

Screening of Chickpea (*Cicer arietinum* L.) Genotypes for Salinity Tolerance Using Agro-physiological Characterization and Genetic ISSR Markers

Abstract:

Two screening experiments (pots and field experiments) were carried on fifty chickpea genotypes under saline and non-saline conditions. The genotypes selected from different location were used for pots experiment to investigate the effect of salinity stress (control, 1500, 300 ppm). Twenty five genotypes selected from pot experiment, with a range of responses to salinity stress were used in the field experiment at two different environments; Ismailia region (non-saline) and El-Arish region (saline) through two successive seasons winter 2016/17 and 2017/18. Results of primarily experiment (pots) were classed genotypes to three groups under 3000ppm (sensitive, moderate and tolerant). Results of the field experiment showed significant difference among genotypes under two environmental conditions. Eight genotypes; Giza1 (G1), Giza195 (G4), FLIP03-27C (G5), FLIP06-65C (G6), 70410 (G9), ILC482C (G18), FLIP06-86C (G20) and Giza4 (G23) showed tolerant response to salinity and give high performance for most growth, yield and biochemical component traits. Relationship among studied traits was indicated to strong correlation (reach to $r = 0.97$) between biochemical components traits and yield traits. Moreover, the highest correlation recorded between 50% flowering and days to maturity ($r = 0.98$). Results of genetic parameters were recorded high values of PCV and GCV under saline condition and non-saline condition for 100 seeds weight, branch number/ plant, filled pods number and pods number/plant traits. Results of genetic advance (GA) showed high value for relative water content (RWC), chlorophyll SPAD value, plant height, pods number, filled pods number and seed weight under saline and non-saline conditions. High values of heritability for most of the agro-physiological traits under both environments indicated that additive gene effects are play an important in inheritance role of these traits. Moreover, ISSR markers were used to differentiate among ten genotypes (tolerant and sensitive); Results showed that the total number of fragments amplified was 103 bands; the polymorphic bands were 47, which represented a level of polymorphism of 45.6%. Moreover, 49 bands were monomorphic and 7 bands were unique amplified DNA fragments ranging from 4 to 13, while the number of polymorphic fragments ranged from 1 to 9 for each primer. A dendrogram separated the ten Chickpea genotypes into two major clusters. Values of genetic similarity ranged from 79% to 93% among the genotypes.